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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=21; hr=9; min=49; sec=55; ms=624;]

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Application No: 10589594

Version No: 3.0

Input Set:

Output Set:

Started: 2008-03-11 13:39:22.927

Finished: 2008-03-11 13:39:23.316

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 389 ms

Total Warnings: 24

Total Errors: 0

No. of SeqIDs Defined: 26

Actual SeqID Count: 26

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (22)

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Error Description

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SEQUENCE LISTING

<110> Nakamura, Yusuke
Furukawa, Yoichi

<120> Method for Diagnosing Colorectal Cancers

<130> 082368-008900US

<140> 10589594

<141> 2008-03-11

<150> WO PCT/JP04/02145

<151> 2004-02-24

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2624

<212> DNA

<213> Homo sapiens

<220>

<223> C10orf3

<220>

<221> CDS

<222> (294)...(1688)

<223> C10orf3

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gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcaccgc gctgggcgcc 240
tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag 344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
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cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa 392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
      20              25              30
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att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga 440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
      35              40              45
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aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc 488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
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ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac				536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp				
	70	75	80	
aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act				584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr				
	85	90	95	
acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg				632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg				
	100	105	110	
agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa				680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys				
	115	120	125	
caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa				728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys				
	130	135	140	145
acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac				776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn				
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tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct				824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala				
	165	170	175	
ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc				872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val				
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tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg				920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr				
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gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca				968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser				
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gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg				1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu				
	230	235	240	
gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag				1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln				
	245	250	255	
ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa				1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln				
	260	265	270	
aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca				1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala				
	275	280	285	

gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa 1208
 Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
 290 295 300 305

aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag 1256
 Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
 310 315 320

aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca 1304
 Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
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tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa 1352
 Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
 340 345 350

caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac 1400
 Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp
 355 360 365

cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga 1448
 Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
 370 375 380 385

aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat 1496
 Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
 390 395 400

gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa 1544
 Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
 405 410 415

aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc 1592
 Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
 420 425 430

aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc 1640
 Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
 435 440 445

act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag 1688
 Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
 450 455 460

caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttggtg 1748
 ggcatatttga attatatatt tcacattttg cataaaactg cctatctacc tttgacactc 1808
 cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgtatc 1868
 ctccctgaca tgggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg 1928
 agactactaa cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcagggttatt 1988
 gctaattgggt taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca 2048
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 cattgaaact taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt 2288
 ttgaggcata atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac 2348
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ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac 2588
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<213> Homo sapiens

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<220>
<223> C10orf3

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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
      35          40          45
Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
      50          55          60
Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
      65          70          75          80
Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
      85          90          95
Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
      100          105          110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
      115          120          125
Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
      130          135          140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
      145          150          155          160
Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
      165          170          175
Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
      180          185          190
Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
      195          200          205
Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
      210          215          220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
      225          230          235          240
Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
      245          250          255
Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
      260          265          270
Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
      275          280          285
Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
      290          295          300
Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
      305          310          315          320
Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
      325          330          335
Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu

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Glu	Asn	Arg	Glu	Lys	Val	Ala	Ala	Ser	Pro	Lys	Ser	Pro	Thr	Ala	Ala
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Leu	Asn	Glu	Ser	Leu	Val	Glu	Cys	Pro	Lys	Cys	Asn	Ile	Gln	Tyr	Pro
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<210> 5
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<220>
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<210> 6
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<220>
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<400> 6
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<210> 8
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<210> 9
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<210> 10
 <211> 22
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<210> 11
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<210> 12
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<220>
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amplification primer for siRNA plasmid vector

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<210> 13
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<212> DNA
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<220>
<223> BamHI and XhoI fragment containing H1RNA PCR
amplification primer

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<210> 14
<211> 29
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<220>
<223> BamHI and XhoI fragment containing H1RNA PCR
amplification primer

<400> 14
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<210> 15
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<220>
<223> PCR amplification primer for ligated DNA template

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<220>
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<210> 17
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<210> 18
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<220>
 <223> C10orf3 siRNA oligonucleotide target sequence

<400> 21
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<210> 22
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> C10orf3 siRNA oligonucleotide hairpin loop structure

<400> 22
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<210> 23
 <211> 488
 <212> DNA
 <213> Artificial

<220>
 <223> psiH1 BX3.0 vector plasmid sequence upstream of siRNA
 DNA fragment insertion site

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 ccactagtaa cggccgccag tgtgctggaa ttcggettgg tagccaagtg cagggttatag 120
 ggagctgaag ggaaggggggt cacagtaggt ggcatcggtc ctttctgact gcccgcccc 180
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 tgtgagggac aggggagtg cgccctgcaa tatttgcatt tcgctatgtg ttctgggaaa 420
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 tctttccc 488

<210> 24
 <211> 4597
 <212> DNA
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<220>
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tccgtgaaac tgcagaaacc caagccgaat tctgcagata